

A32 32, 34, 36, 38, 40, 45-85, 94-111, 125-150, 160-164, 175-178 and
183-264.

A33 98. (Amended) A method for providing a therapeutic G protein coupled receptor signaling modifier peptide to a mammal which comprises administering to said mammal an expression construct which expresses a peptide according to SEQ ID NOS: 2, 4, 6, 8, 10, 12, 13, 15, 17, 21, 23, 25-27, 30, 32, 34, 36, 38, 40, 45-85, 94-111, 125-150, 160-164, 175-178 and 183-264.

REMARKS

Applicants request that the amendments specified herein and the accompanying initial Sequence Listing be entered prior to examination on the merits. The amendments correct inconsistencies in the sequence identification numbering, very minor typographical errors, and priority information from prior copending provisional application 60/275,472, filed March 14, 2001. The amendments contain no new matter.

Applicants are providing the Sequence Listing in both computer-readable form and paper copy. Applicants hereby state that the information on the computer-readable disk and the paper copy are the same and contain no new matter.

Applicants respectfully request examination on the merits and favorable consideration.

RESPECTFULLY SUBMITTED,					
NAME AND REG. NUMBER	Martha Cassidy Registration No. 44,066				
SIGNATURE			DATE	9/17/01	
Address	Rothwell, Figg, Ernst & Manbeck Suite 701-East, 555 13th Street, N.W.				
City	Washington	State	D.C.	Zip Code	20004
Country	U.S.A.	Telephone	202-783-6040	Fax	202-783-6031

Attachment: Mark-up of Specification and Claims

Mark-up of the Specification:

On page 6, paragraph 0011:

These [finding] findings have led to a modification of traditional receptor theory (Samama et al., J. Biol. Chem. 268:4625-4636, 1993). It is now thought that receptors can exist in at least two conformations, an inactive conformation (R) and an activated conformation (R*), and that an equilibrium exists between these two states that markedly favors R over R* in the majority of receptors. It has been proposed that in some native receptors and in the mutants described above, there is a shift in equilibrium in the absence of agonist that allows a sufficient number of receptors to be in the active R* state to initiate signaling.

On page 11, paragraph 0020:

The invention provides, in yet a further embodiment a compound selected from the group consisting of SEQ ID NOS:[14, 16, 20, 22, 26, 28, 30, 32, 34, 36, 38, 40, 42, 46-105, 115-132 and 147-305] 2, 4, 6, 8, 10, 12, 13, 15, 17, 21, 23, 25-27, 30, 32, 34, 36, 38, 40, 45-85, 94-111, 125-150, 160-164, 175-178 and 183-264.

On page 11, paragraph 0021:

In yet a further embodiment, the invention provides a method for providing a therapeutic G protein coupled receptor signaling modifier peptide to a mammal which comprises administering to said mammal an expression construct which expresses a peptide according to SEQ ID NOS:[14, 16, 20, 22, 26, 28, 30, 32, 34, 36, 38, 40, 42, 46-105, 115-132 and 147-305] 2, 4, 6, 8, 10, 12, 13,

15, 17, 21, 23, 25-27, 30, 32, 34, 36, 38, 40, 45-85, 94-111,
125-150, 160-164, 175-178 and 183-264.

On page 12, paragraph 0028:

Figure 7 is a bar graph showing competitive inhibition of high affinity peptides to rhodopsin by [heterotrimeric] heterotrimeric Gt.

On page 12, paragraph 0029:

Figure 8 presents ELISA results from panning CHO cells overexpressing human thrombin receptor (PAR1) using purified MBP-C-terminal fusion proteins. MBP-G11 = xxxx (SEQ ID NO: 1) LQLNLKEYNLV (SEQ ID NO: 2); PAR-13 = VRPS (SEQ ID NO: 3) LQLNRNEYYLV (SEQ ID NO: 4); PAR-23 = LSRS (SEQ ID NO: 5) LQQKLKEYSLV (SEQ ID NO: 6); PAR-33 = LSTN (SEQ ID NO: 7) LHNLKEYNLV (SEQ ID NO: 8); PAR-34 = LPQM (SEQ ID NO: 9) QRLNVGEYNLV (SEQ ID NO: 10); PAR-45 = SRHT (SEQ ID NO: 11) LRLNGKELNLV (SEQ ID NO: [194]12).

Table I, bridging pages 22 and 23:

Table I. Example for Construction of a Synthetic Peptide Library.

Q R M H L R Q Y E L L (SEQ ID NO:13)
gaggttgtt nnknnknnknnk attcgtaaaaacttaaaagattgtggtcgtttc taa ctaagtaaagc
A B C D E

(SEQ ID NO: [12]14) n = any [amino acid]nucleotide base; k = guanidine or thymidine; A = restriction enzyme site; B = linker sequence; C = oligonucleotide encoding peptide sequence [SEQ ID NO:13]; D = stop codon; E = restriction enzyme site.

On page 23, Table II:

Table II. $\text{G}\alpha$ Subunit Peptides and Corresponding DNA Constructs.

<u>$\text{G}\alpha$ Subunit</u>	<u>Sequence</u>													<u>SEQ ID NO:</u>
Gt	I atc	K aag	E gag	N aac	L ctg	K aaa	D gac	C tgc	G ggc	L ctc	F ttc		[14] <u>15</u> [15] <u>16</u>	
Gi1/2	I ata	K aaa	N aat	N aat	L cta	K aaa	D gat	C tgt	G ggt	L ctc	F ttc		[16] <u>17</u> [17] <u>18</u>	
GRi1/2	N aac	G ggc	I atc	K aag	C tgc	L ctc	F ttc	N aac	D gac	K aag	L ctg		[18] <u>19</u> [19] <u>20</u>	
Gi3	I att	K aaa	N aac	N aac	L tta	K aag	E gaa	C tgt	G gga	L ctt	Y tat		[20] <u>21</u> [21] <u>22</u>	
Go2	I atc	A gcc	K aaa	N aac	L ctg	R cgg	G ggc	C tgt	G gga	L ctc	Y tac		[22] <u>23</u> [23] <u>24</u>	
Go1	I att	A gcc	N aac	N aac	L ctc	R cgg	G ggc	C tgc	G ggc	L ttg	Y tac		[24] <u>25</u> [25] <u>26</u>	
Gz	I ata	Q cag	N aac	N aat	L ctc	K aag	Y tac	I att	G ggc	L ctt	C tgc		[26] <u>27</u> [27] <u>28</u>	
G11	L ctg	Q cag	L ctg	N aac	L ctc	K aag	E gag	Y tac	N aac	L ctg	V gtc		[28] <u>2</u> 29	
Gq	L ctc	Q cag	L ttg	N aac	L ctg	K aag	E gag	Y tac	N aat	A gca	V gtc		30 31	
Golf	Q cag	R cg	M atg	H cac	L ctc	K aag	Q cag	Y tat	E gag	L ctc	L ttg		32 33	
G14	L cta	Q cag	L cta	N aac	L cta	R agg	E gaa	F ttc	N aac	L ctt	V gtc		34 35	
G15/16	L ctc	A gcc	R cgc	Y tac	L ctg	D gac	E gag	I atc	N aac	L ctg	L ctg		36 37	
G12	L ctg	Q cag	E gag	N aac	L ctg	K aag	D gac	I atc	M atg	L ctg	Q cag		38 39	
G13	L ctg	H cat	D gac	N aac	L ctc	K aag	Q cag	L ctt	M atg	L cta	Q cag		40 41	
Gs	Q cag	R cg	M atg	H cac	L ctt	R cgt	Q cag	Y tac	E gag	L ctg	L ctc		[42] <u>13</u> [43] <u>42</u>	
5' - gatccggccaccatggga-														-tgaa-3'

(SEQ ID NOS: [44]43, [45]44)

On pages 24-25, Table III:

Table III. Exemplary Native G Protein Sequences for Library or Minigene Construction.*

Name	Sequence	SEQ ID NO:	Name	Sequence	SEQ ID NO:
[hgt]hGt	IKENLKDGLF	[46]15	CryptoGbal	LQNALRDSGIL	[76]62
hGi1/2	IKNNLKDGLF	[47]17	GA3_UST	LTNALKDSGIL	[77]63
G05_DRO	IKNNLKQIGLF	[48]45	GA1_KLU	IQQNLKKSGIL	[78]64
GAF_DRO	LSENVSSMGLF	[49]46	GA3_UST	LTNALKDSGIL	[79]63
Gi-DRO	IKNNLKQIGLF	[50]45	GA1_DIC	NLTGEAGMIL	[80]64
hGi3	IKNNLKECGLY	[51]21	GA2_KLU	LENSLKDSGVL	[81]65
hGO-1	IANNLRGCGLY	[52]25	GA2_UST	ILTNNLRDIVL	[82]66
hGO-2	IAKNLRGCGLY	[53]47	Mgs-XL	ORMHLPQYELL	[83]67
GAK_CAV	IKNNLKECGLY	[54]21	hGs	ORMHHLRQYELL	[84]13
G0_XEN	IAYNLRGCGLY	[55]48	hGolf	ORMHLKGYELL	[85]68
GA3_CAEEL	IQANLQGCGLY	[56]49	GA1_COPCO	LQLHLRECGLL	[86]69
GA2_CAEEL	IQSNLHKSGLY	[57]50	GA1-SOL	RRRNLFAGLL	[87]70
GA1_CAEEL	LSTKLKGCGLY	[58]51	GA2_SB	RRRNLLAEAGLL	[88]71
GAK_XEN	IKSNILMECGLY	[59]52	GA1_SB	RRRNPLEAGLL	[89]72
GA1_CAN	VQQNLKKSGIM	[60]53	GA1_UST	IQVNLRDCGLL	[90]73
hGZ	IQNNLKYIGLC	[61]27	GA4_UST	RENLKLTGLVG	[91]74
hG15	LARYLDEINLL	[62]26	GA1_ORYSA	DESMRRSREGT	[92]75
GA2_SCHPO	LQHSLKEAGMF	[63]54	GQ1_DROME	MQNALKEFNLG	[93]76
hG12	LQENLKDIMLQ	[64]38	GA2_DIC	TQCVMKAGLYS	[94]77
hG13	LHDNLKQLMLQ	[65]40	GS-SCH	LQHSLKEAGMF	[95]54
GAL_DRO	LQRNLNALMLQ	[66]55	GA-SAC	ENTLKDSGVLQ	[96]56
GA2_YST	ENTLKDSGVLQ	[67]56	GA1-CE	IISASLKMVGV	[97]78
hG14	LQLNLREFNLV	[68]34	GA2-CE	NENLRSAGLHE	[98]79
hG11	LQLNLKEYNLV	[69]2	GA3-CE	RLIRYANNIPV	[99]80
hGQ	LQLNLKEYNAV	[70]30	GA4-CE	LSTKLKGCGLY	[100]51
GQ_DROME	LQSNLKEYNLV	[71]57	GA5-CE	IAKNLKSMGLC	[101]81
G11_XEN	LQHNLKEYNLV	[72]58	GA6-CE	IGRNLRGTGME	[102]82
Gq_SPOSC	IQENLRLCGLI	[73]59	GA7-CE	IQHTMQKVGIQ	[103]83
GA1_YST	IQQNLKKIGII	[74]60	GA8-CE	IQKNLQKAGMM	[104]84
GA1_NEUCR	IIQRNLKQLIL	[75]61	GA5-DIC	LKNIFNTIINY	[105]85

*For production of minigene constructs each nucleotide sequence should be constructed to encode the amino acids MG at the N-terminus of the peptide by using 5'-gatccggccaccatggaa-(SEQ ID NO:[44]43) and -tcaa-3' (SEQ ID NO:[45]44).

On page 29 Table IV:

Table IV. Diversity in Unpanned Gq Library.

		SEQ. ID NO.
Native	LQLNLKEYNLV	[106] <u>2</u>
clone #1	LLLQLVEHTLV	[107] <u>86</u>
clone #2	HRLNLLEYCLV	[108] <u>87</u>
clone #3	EQWMNMNTFHMI	[109] <u>88</u>
clone #4	SQVKLQKGHLV	[110] <u>89</u>
clone #5	LRLLL*EYNLG	[111] <u>90</u>
clone #6	RRLKVNEYKLL	[112] <u>91</u>
clone #7	LQLRLREHNLV	[113] <u>92</u>
clone #8	HVLNSKEYNQV	[114] <u>93</u>

On page 30, Table V:

Table V. Selection in Panned Gα11 Library.

		SEQ ID NO.
Native	LQLNLKEYNLV	[106] <u>2</u>
<i>Round 1</i>		
1	MKLNVSESNLV	[115] <u>94</u>
2	LQTNQKEYDMD	[116] <u>95</u>
3	LQLNPREDKLW	[117] <u>96</u>
4	RHLDLNACNMG	[118] <u>97</u>
5	LR*NDIEALLV	[119] <u>98</u>
6	LVQDRQESILV	[120] <u>99</u>
<i>Round 2</i>		
1	LQLKHKENNLM	[121] <u>100</u>
2	LQVNLEEYHLV	[122] <u>101</u>
3	LQFNLNDCNLV	[123] <u>102</u>
4	MKLKLKEDNLV	[124] <u>103</u>
5	HQLDLLEYNLG	[125] <u>104</u>
6	RLDFSEKQLV	[126] <u>105</u>
<i>Round 3</i>		
1	LQKNLKEYNMV	[127] <u>106</u>
2	LQYNLMEDYLN	[128] <u>107</u>
3	LQMYLRGYNLV	[129] <u>108</u>
4	LPLNPKEYSLV	[130] <u>109</u>
5	MNLTLKECNLV	[131] <u>110</u>
6	LQQSLIEYNLL	[132] <u>111</u>

On page 43 Table VI:

Table VI. Exemplary Sequences of C-terminal Minigene Peptides.

Peptide Name	Sequence	SEQ ID NO:
G α i	MGIKNNLKDCGLF	[133] <u>112</u>
G α iR	MGNGIKCLFNDKL	[134] <u>113</u>
G α q	MGLQLNLKEYNAV	[135] <u>114</u>
G α q**	MGLQLNLKEYNTL	[136] <u>115</u>
G α 12	MGLQENLKDIMLQ	[137] <u>116</u>
G α 13	MGLHDNLKQLMLQ	[138] <u>117</u>

Paragraph 0100, bridging pages 49 and 50:

Construction of a biased peptide library has been described previously. Martin et al., *J. Biol. Chem.* 271:361-366, 1996; Schatz et al., *Meth. Enzymol.* 267:171-191, 1996. The vector used for library construction was pJS142 (see Figure 2). This vector had a linker sequence between the LacI and the biased [undercamer] undecamer peptide coding sequence, as well as restriction sites for cloning the library oligonucleotide. The oligonucleotide synthesized to encode the mutagenesis library was synthesized with 70% of the correct base and 10% of each of the other bases at each position. This mutagenesis rate leads to a biased library such that there is approximately a 50% chance that any of the 11 codons will be the appropriate amino acid and approximately a 50% chance that it will be another amino acid. In addition, a linker of four random NNK (where N denotes A, C, G or T and K denotes G or T) codons were synthesized at the 5' end of the sequence to make a total of 15 randomized codons. Using this method, a library with greater than 10^9 independent clones

per microgram of vector used in the ligation was constructed based on the carboxyl terminal sequence of G α t (IKENLKDCGLF; SEQ ID NO: [139] 15). The nucleic acid used for creating this library was: [5'-]

5'-GAGGTGGTNNKNNKNNKNNKattcaaggagaacctgaaggactgcggcctttCTAACTAAGTAAAGC-3', wherein N= A/C/G/T and K= G/T; SEQ ID NO: [140] 118).

On page 50, Table VI:

Table [VI]VII. C-Terminal G α Subunit Peptide Library Constructs.

G α Sub-unit	RE	Linker	Peptide Coding Region	Stop	RE	SEQ ID NO:
Gs	5-GAGGTGGT	NNKNNKNNKNNK	attcgtgaaaacttaaaagattgtggtcgttc	TAA	CTAAGTAAAGC-3'	[141] 14
G11	5-GAGGTGGT	NNKNNKNNKNNK	ctgcagctgaacctgaaggagtacaatctggtc	TAA	CTAAGTAAAGC-3'	[142] 119
G12	5-GAGGTGGT	NNKNNKNNKNNK	ctgcaggagaacctgaaggacatcatgctgcag	TAA	CTAAGTAAAGC-3'	[143] 120
G13	5-GAGGTGGT	NNKNNKNNKNNK	ctgcatgacaacctcaagcagcgttatgctacag	TAA	CTAAGTAAAGC-3'	[144] 121
G15	5-GAGGTGGT	NNKNNKNNKNNK	ctcgcccggtacctggacgagattaatctgctg	TAA	CTAAGTAAAGC-3'	[145] 122
Gz	5-GAGGTGGT	NNKNNKNNKNNK	atacagaacaatctcaagtacattggccttc	TAA	CTAAGTAAAGC-3'	[146] 123

On page 58, paragraph 0114:

The panning process is illustrated in Figure 1. For screening of the library by "panning," rhodopsin receptors prepared according to Example 5 were immobilized directly on Immulon 4 (Dynatech) microtiter wells (0.1-1 μ g of protein per well) in cold 35 mM HEPES, pH 7.5, containing 0.1 mM EDTA, 50 mM KCl and 1mM [dithiothriitol]dithiothreitol (HEK/DTT). After shaking for one hour at 4°C, unbound membrane fragments were washed away with HEK/DTT. The wells were blocked with 100 μ l 2% BSA in HEKL (35 [Mm] mM HEPES; [0.1 mM] 0.1 mM EDTA; 50 mM KCl; 0.2 M α -lactose; pH 7.5, with 1 mM DTT). For rounds 1 and 2, BSA was used for blocking; in later rounds 1% nonfat dry milk was used. For the first round of panning, about 24 wells of a 96-well plate were used. In subsequent rounds, 8 wells with receptor and 8 wells without receptor were prepared.

On page 61, Table IX:

Table IX. Light-Activated Rhodopsin High Affinity Sequences.

Clone No.	SEQ ID NO:	Sequence
Library Sequence	[139] <u>124</u>	[I R E N L K D C G L F] <u>IRENLKDCGLF</u>
8	[147] <u>125</u>	[L L E N L R D C G M F] <u>LLENLRDCGMF</u>
9	[148] <u>126</u>	[I Q G V L K D C G L L] <u>IQGVLKDCGLL</u>
10	[149] <u>127</u>	[I C E N L K E C G L F] <u>ICENLKECGLF</u>
18	[150] <u>128</u>	[M L E N L K D C G L F] <u>MLENLKDCGLF</u>
23	[151] <u>129</u>	[V L E D L K S C G L F] <u>VLEDLKSCGLF</u>
24	[152] <u>130</u>	[M L K N L K D C G M F] <u>MLKNLKDCGMF</u>
3	[153] <u>131</u>	[L L D N I K D C G L F] <u>LLDNIKDCGLF</u>
4	[154] <u>132</u>	[I L T K L T D C G L F] <u>ILTKLTDCGLF</u>
6	[155] <u>133</u>	[L R E S L K Q C G L F] <u>LRESLKQCGLF</u>
11	[156] <u>134</u>	[I H A S L R D C G L F] <u>IHASLRDCGLF</u>
13	[157] <u>135</u>	[I R G S L K D C G L F] <u>IRGSLKDCGLF</u>
14	[158] <u>136</u>	[I F L N L K D C G L F] <u>IFLNLKDCGLF</u>
15/28	[159] <u>137</u>	[I R E N L E D C G L F] <u>IRENLEDCGLF</u>
16	[160] <u>138</u>	[I I D N L K D C G L F] <u>IIDNLKDCGLF</u>
17	[161] <u>139</u>	[M R E S L K D C G L F] <u>MRESLKDCGLF</u>
19	[162] <u>140</u>	[I R E T L K D C G L L] <u>IRETLKDCGLL</u>
26	[163] <u>141</u>	[I L A D V I D C G L F] <u>ILADVIDCGLF</u>
27	[164] <u>142</u>	[M C E S L K E C G L F] <u>MCESLKECGLF</u>

On page 62, Table X:

Table X. Dark-Adapted Rhodopsin High Affinity Sequences.

Clone No.	SEQ ID NO:	Sequence
Library Sequence	[139] <u>124</u>	[I R E N L K D C G L F] <u>IRENLKDCGLE</u>
2	[165] <u>143</u>	[I R E K W K D L A L F] <u>IREWKWDLALF</u>
3	[166] <u>144</u>	[V R D N L K N C F L F] <u>VRDNLKNCFLF</u>
7	[167] <u>145</u>	[I G E Q I E D C G P F] <u>IGEQIEDCGPF</u>
17	[168] <u>146</u>	[I R N N L K R Y G M F] <u>IRNNLKRYGMF</u>
21	[169] <u>147</u>	[I R E N L K D L G L V] <u>IRENLKDLGLV</u>
26	[170] <u>148</u>	[I R E N F K Y L G L W] <u>IRENFKYLGW</u>
33/37	[171] <u>149</u>	[S L E I L K D W G L F] <u>SLEILKDWGLF</u>
41	[172] <u>150</u>	[I R G T L K G W G L F] <u>IRGTLKGWGLF</u>

On page 62, paragraph 0118:

The methods of Example 7 were used to screen different sources of PAR1 receptor using the Gq library. Purified PAR1, reconstituted in lipid vesicles (Example 6), membranes prepared from Sf9 insect cells expressing PAR1 (Example 2) and membranes prepared from mammalian cells overexpressing PAR1 were used. The results of the screens are presented in Tables XI, XII and XIII, respectively. The peptide used as the competitor was LQLNLKEYNLV (SEQ ID NO:[56]2).

On Page 63, Table XI:

Table XI. Reconstituted Purified Recombinant PAR1 Receptor; Screening Results.

Clone		SEQ ID NO:	SEQ ID NO:
R2-16	*SWV	[319] <u>151</u>	LQFNLNDNLV [173] <u>102</u>
R2-17	FVNC	[320] <u>152</u>	LQRNKKQYNLG [174] <u>160</u>
R2-18	EVRR	[321] <u>153</u>	MKLKLKEDNLV [175] <u>103</u>
R2-20	*RVQ	[322] <u>154</u>	HQLDLLEYNLG [176] <u>104</u>
R2-21	RLTR	[323] <u>155</u>	LQLRYKCYNLV [177] <u>161</u>
R3-37	SR*K	[324] <u>156</u>	LQQSLIEYNLL [178] <u>111</u>
R3-38	MTHS	[325] <u>157</u>	VHVKLKEYNLV [179] <u>162</u>
R3-44	SGPQ	[326] <u>158</u>	LQLNVKEYNLV [180] <u>163</u>
R3-46	ML*N	[327] <u>159</u>	LRIYLKGYNLV [181] <u>164</u>

On Page 63, Table XII:

Table XII. PAR1 Receptor Sf9 Insect Cell Membranes; Screening Results.

Clone		SEQ ID NO:	SEQ ID NO:
S1-13	S*IR	[328] <u>165</u>	MKLNVSESNLV [182] <u>94</u>
S1-18	RWIV	[329] <u>166</u>	LQLNLKVYNLV [183] <u>175</u>
S1-23	G*GH	[330] <u>167</u>	LELNLKVYNLF [184] <u>176</u>
S2-26	RSEV	[331] <u>168</u>	LQLKHKENNL [185] <u>100</u>
S2-30	CEPG	[332] <u>169</u>	LHLNMAEVSLV [186] <u>177</u>
S2-36	HQMA	[333] <u>170</u>	LQVNLEEYHLV [187] <u>101</u>
S3-6	VPSP	[334] <u>171</u>	LQKNLKEYNMV [188] <u>106</u>
S3-8	QMPN	[335] <u>172</u>	LQMYLRGYNLV [189] <u>108</u>
S3-10	MWPS	[336] <u>173</u>	LKRYLKESNLV [190] <u>178</u>
S3-15	C*VE	[337] <u>174</u>	MNLTLKECNLV [191] <u>110</u>

On page 63, Table XIII:

Table XIII. Mammalian (CHO) Cells Overexpressing PAR1; Screening Results.

Clone		SEQ ID NO:	SEQ ID NO:
C4-5	PRQL	[338] <u>179</u>	LQLKRGEYILV [192] <u>183</u>
C4-19	VRPS	[339] <u>3</u>	LQLNRNEYYLV [193] <u>3</u>
C5-10	SRHT	[340] <u>11</u>	LRLNGKELNLV [194] <u>12</u>
C5-12	FFWV	[341] <u>180</u>	CSLKLKAYNLV [195] <u>184</u>
C4-16	ORDT	[342] <u>181</u>	LQMHNEYNLV [196] <u>185</u>
C7-3	NFRN	[343] <u>182</u>	PQLNLNAYNLV [197] <u>186</u>
C7-10	LPQM	[344] <u>9</u>	QRLNVGEYNLV [198] <u>10</u>
C7-13	LSTN	[345] <u>7</u>	LHNLKEYNLV [199] <u>8</u>
C7-14	LSRS	[346] <u>4</u>	LQQKLKEYSLV [200] <u>6</u>

On page 64, Table XIV:

Table XIV. β 2-Adrenergic Receptor screened with Gs library.
SEQ ID NO:

Competitor	Sequence	SEQ ID NO:	ELISA
AG1	QGMQLRRFKLR	[201] <u>187</u>	.435
AG20	RWLHWQYRGRG	[202] <u>188</u>	.431
AG19	PRPRLLRFKIP	[203] <u>189</u>	.361
AG2	QGEHLRQLQLOQ	[204] <u>190</u>	.330
AG4	QRLRLGPDELF	[205] <u>191</u>	.291
BAR1	QRIHRRPKFF	[206] <u>192</u>	.218
AG3	QRMPLRLFEFL	[207] <u>193</u>	.217
BAR2	QRVHLRQDELL	[208] <u>194</u>	.197
AG11	DRMHLWRFGLL	[209] <u>195</u>	.192
AG9	QRMPLRQYELL	[210] <u>196</u>	.190
BAR3	QWMDLRLQHELL	[211] <u>197</u>	.185
AG18	QRMNLGPCGLL	[212] <u>198</u>	.155
BAR20	NCMKFRSCGLF	[213] <u>199</u>	.079
AG13	QRLHLRGYEF	[214] <u>200</u>	.054
BAR11	HRRHIGPFALL	[215] <u>201</u>	.048
BAR8	ERLHRLFQLH	[216] <u>202</u>	.047
BAR40	PCIQLGQYESF	[217] <u>203</u>	.028
BAR31	QRLRLRKYRLF	[218] <u>204</u>	.026

On page 65, Table XV:

Table XV. Rhodopsin screened with Gt library.

Competitor	SEQ ID NO:	ELISA
	IRENLKDCGLF	[14] <u>124</u>
L33	IVEILEDCGLF	[219] <u>205</u>
L4	MLDNLKACGLF	[220] <u>206</u>
L3	ILENLKDCGLF	[221] <u>207</u>
L14	LRENLKDCGLL	[222] <u>208</u>
L38	LLDILKDCGLF	[223] <u>209</u>
L15	VRDILKDCGLF	[224] <u>210</u>
L34	ILESILNECGLF	[225] <u>211</u>
L17	ILQNLKDCGLF	[226] <u>212</u>
L7	MLDNLKDCGLF	[227] <u>213</u>
L10	IHDRLKDCGLF	[228] <u>214</u>
L20	IRGSLKDCGLF	[229] <u>135</u>
L6	ICENLKDCGLF	[230] <u>215</u>
L8	IVKNLEDCGLF	[231] <u>216</u>
L13	ISKNLRDCGLL	[232] <u>217</u>
L10	IRDNLKDCGLF	[233] <u>218</u>

On page 66, paragraph 0120:

Chinese hamster ovary-expressed PAR1 was screened against the Gt, G12 and G13 libraries, using the competitor peptide indicated in Table XVI below. Additional peptide analogs were identified using the G11 library and LQLNLKEYNLV (SEQ ID NO:[243]2) as competitor and screened for high affinity binding to PAR1 receptor obtained from different sources, indicated in Table XVII, below.

On Page 66, Table XVI:

Table XVI. Peptides Identified with CHO EXPRESSED PAR1.

Gt library (IRENLKDCGLF; SEQ ID NO:[14]124)	G12 library (LQENLKDIMLQ; SEQ ID NO:[64]38)	G13 library (LQDNLKQLMLQ; SEQ ID NO:[65]233)
IREFLTDGGLF [234]219	LQENLKEMMLQ [240]225	LQDNLRHMLQ [248]234
IRLDLKDVSLF [235]220	LEENLKYRMLD [241]226	LQDKINHMLQ [249]235
ICERLNDCGLC [236]221	LQEDLKGMTLQ [242]227	LQANRKLGMLQ [250]236
PRDNTKVRGLF [237]222	LQETMKDQSLQ [243]228	LIVKVKQLIWQ [251]237
FWGNLQDSGLF [230]223	PQVNLSIMRQ [244]229	MRAKLNNLMLQ [252]238
RRGNGKDCRHF [239]224	WQHKLSEVMLQ [245]230	LQDNLRHLIQ [253]239
	LKEHLMERMLQ [246]231	LQDNRNQLLF [254]240
	LLGMLEPLMEQ [247]232	

On page 67 Table XVII:

Table XVII. PAR1 Binding Peptides Screened using a G11 Library (LQLNLKEYNLV; SEQ ID NO: 2)

CHO EXPRESSED	SEQ ID NO:	Recomb/Reconst	SEQ ID NO:	SF9 EXPRESSED	SEQ ID NO:
LQLNVKEYNLV	[255] <u>163</u>	LQLNVKEYNLV	[275] <u>163</u>	LQLNLKVYNLV	[289] <u>175</u>
LQLNRKKNYNLV	[256] <u>241</u>	LQLRVKEYKRG	[276] <u>244</u>	LQLKHKENNLM	[290] <u>100</u>
LQLRYKCYNLV	[257] <u>161</u>	LQLRYKCYNLV	[277] <u>161</u>	LQKNLKEYNMV	[291] <u>106</u>
LQLDLKESNMV	[258] <u>242</u>	LQIYLKGYNLV	[278] <u>245</u>	LQVNLEEYHLV	[292] <u>101</u>
LQLNLKKYNRV	[259] <u>243</u>	LQFNLNDCNLV	[279] <u>102</u>	LFLNLKEYSLV	[293] <u>257</u>
LQLRVKEYKRG	[260] <u>244</u>	LQRNKKQYNLG	[280] <u>160</u>	LELNLKVYNLV	[294] <u>258</u>
LQRNKKQYNLG	[261] <u>160</u>	LQRNKNQYNLG	[281] <u>254</u>	LPLNPKEYSLV	[295] <u>109</u>
LQIYLKGYNLV	[262] <u>245</u>	LQQSLIEYNLL	[282] <u>111</u>	LPLNLIDFSLM	[296] <u>259</u>
LQFNLNDCNLV	[263] <u>102</u>	LRLDLSEKQLV	[283] <u>105</u>	LPRNLKEYDLG	[297] <u>260</u>
LQYNLKESFVV	[264] <u>246</u>	LYLDLKEYCLF	[284] <u>255</u>	LRLNDIEALLV	[298] <u>261</u>
LQQSLIEYNLL	[265] <u>111</u>	HQLDLLEYNLG	[285] <u>104</u>	LVLNRIEYNLL	[299] <u>262</u>
LQRDHVEYKLF	[266] <u>247</u>	VQVKLKEYNLV	[286] <u>251</u>	LHLNMAEVSLV	[300] <u>177</u>
LVIKPKEFNLV	[267] <u>248</u>	MKLKLKEDNLV	[287] <u>103</u>	MNLTLKECNLV	[301] <u>110</u>
IQLNLKNYNIV	[268] <u>249</u>	SAKELDQYNLG	[288] <u>256</u>	MKLNVSESNLV	[302] <u>94</u>
HQLDLLEYNLG	[269] <u>104</u>			LKRYLKESNLV	[303] <u>178</u>
MQLNLKEYNLV	[270] <u>250</u>			LKRKLKESNMG	[304] <u>263</u>
VQVKLKEYNLV	[271] <u>251</u>			LKRKVKEYNLG	[305] <u>264</u>
QLLNQYVYNLV	[272] <u>252</u>				
MKLKLKEDNLV	[273] <u>103</u>				
WRLSLKVYNLV	[274] <u>253</u>				

Paragraph 0121, bridging pages 67 and 68:

In the last round of panning, several clones were selected from the (+) receptor plates and grown up overnight in LB-Amp media. Three hundred microliters of the overnight culture was diluted in 3 mL in LB-Amp media for "ELISA lysate culture." Another 30 μ L was added to an equal volume of 50% glycerol was stored in labeled microcentrifuge tubes at -70°C. The remaining 4.5 mL was used to make DNA using a standard miniprep protocol

(Qiagen Spinprep™ kits) and sequenced using a 19 base pair reverse primer which is homologous to the vector at a site 56 basepairs downstream from the TAA stop codon that terminates the random region of the library (GAAAATCTTCTCTCATCCG; SEQ ID NO: [306]265). The DNA was stored at -20°C. The ELISA lysate culture was allowed to shake for one hour at 37°C. Expression was induced by adding 33 µL 20% arabinose (0.2% final concentration) with shaking at 37°C for 2-3 hours. The culture then was subjected to sedimentation at 4000 xg for five minutes, the pellet resuspended in 3 mL cold WTEK buffer, resedimented at 4000 xg for five minutes and the pellet resuspended in 1 mL cold TEK buffer. After transfer to 1.5 mL microcentrifuge tubes, the pellet was sedimented at 13,000 xg for two minutes and the supernatant aspirated. The cell pellet was resuspended in 1 mL lysis buffer (42 mL HE, 5 mL 50% glycerol, 3 mL 10 mg/mL BSA in HE, 750 µL 10 mg/mL lysozyme in HE and 62.5 µL 0.2 M PMSF) and incubated on ice for one hour. One hundred ten microliters 2M KCl was added to the lysis mixture and inverted to mix, then sedimented at 13,000 xg for 15 minutes at 4°C. The clear crude lysate (about 0.9 mL supernatant) was transferred to a new tube and stored at -70°C.

Paragraph 0123, bridging pages 69 and 70:

To identify peptides having even higher affinity to light-activated rhodopsin than those identified by the panning procedure described in Example 7, a high affinity peptide was included in the library incubations in rounds three and four.

Peptide 8 (LLENLRDCGMF; SEQ ID NO:[147]125) had been identified in the first screening as a peptide exhibiting binding to light-activated rhodopsin 1000-fold higher than the native sequence. Screening of the G α library was performed as in Example 7, except that 10 μ L 100 μ M (100 nM final concentration) peptide 8 was included in the wells in rounds three and four. This screen revealed several clones that both bind rhodopsin with very high affinity and stabilize it in its active form, metarhodopsin II. See Table XVIII, below. Comparing Tables IX and XVIII, it is clear that the use of peptide 8 in the screen resulted in a change at position 341 to a neutral residue. Residues L344, C347 and G348 remained stable whether peptide 8 was included in the screen or not. Use of peptide 8 resulted in a higher incidence of isoleucine at position 340 (17% with native peptide versus 71% with peptide 8) and a lower incidence of glutamine at position 342 (67% with native peptide versus 29% with peptide 8). This type of information not only contributes to the discovery of highly potent analog peptides for use as drugs or drug screening compounds, but also furthers the understanding of the structural framework which underlies the sites of contact between G α and receptor.

On page 71, Table XVIII:

Table XVIII. Exemplary Light-Activated Rhodopsin High Affinity Sequences Identified in Screens with Addition of Peptide 8.

Clone No.	SEQ ID NO:	Sequence
Library Sequence	[14] <u>124</u>	[I R E N L K D C G L F] <u>IRENLKDCGLF</u>
Peptide 8	[147] <u>125</u>	[L L E N L R D C G M F] <u>LLENLRDCGMF</u>
3	[307] <u>266</u>	[I L E N L K D C G L L] <u>ILENLKDCGLL</u>
7	[308] <u>213</u>	[M L D N L K D C G L F] <u>MLDNLKDCGLF</u>
8	[309] <u>216</u>	[I V K N L E D C G L F] <u>IVKNLEDCGLF</u>
10	[310] <u>218</u>	[I R D N L K D C G L F] <u>IRDNLKDCGLF</u>
13	[311] <u>217</u>	[I S K N L R D C G L L] <u>ISKNLRDCGLL</u>
17	[312] <u>212</u>	[I L Q N L K D C G L F] <u>ILQNLKDCGLF</u>
19	[313] <u>206</u>	[M L D N L K A C G L F] <u>MLDNLKACGLF</u>

Paragraph 0136, bridging pages 78 and 79:

cDNA encoding the last 11 amino acids of G α subunits was synthesized (Great American Gene Company) with newly engineered 5'- and 3'- ends. The 5'- end contained a BamHI restriction enzyme site followed by the human ribosome-binding consensus sequence (5'- GCCGCCACC-3'; SEQ ID NO:[314]267), a methionine codon (ATG) for translation initiation, and a glycine codon (GGA) to protect the ribosome binding site during translation and the nascent peptide against proteolytic degradation. A HindIII restriction enzyme site was synthesized at the 3' end immediately following the translational stop codon (TGA). Thus, the full-length 56 bp oligonucleotide for the G $\alpha_{1/2}$ carboxyl terminal sequence was

5'-gatccggccgccaccatggaatcaagaacaacctgaaggactgcggcctttctgaa -3'
(SEQ ID NO:[315]268) and the complimentary strand was
5'-agctttcagaagaggccgcagtcctcaggttgttattccatggtggcggcg-3'
(SEQ ID NO:[316]269). See Figure 11. As a control,
oligonucleotides encoding the $\text{G}\alpha_{i1/2}$ carboxyl terminus in random
order ($\text{G}\alpha_{iR}$) with newly engineered 5'- and 3'- ends also were
synthesized. The DNA was diluted in sterile ddH₂O to form a
stock concentration at 100 μM . Complimentary DNA was annealed
in 1X NEBuffer 3 (50 mM Tris-HCl, 10 mM MgCl₂, 100 mM NaCl, 1 mM
DTT; New England Biolabs) at 85 °C for 10 min then allowed to cool
slowly to room temperature. The DNA then was subjected to 4%
agarose gel electrophoresis and the annealed band was excised.
DNA was purified from the band using a kit, according to the
manufacture's protocol (GeneClean II Kit, Bio101). After
digestion with each restriction enzyme, the pcDNA 3.1(-) plasmid
vector was subjected to 0.8% agarose gel electrophoresis, the
appropriate band cut out, and the DNA purified as above
(GeneClean II Kit, Bio101). The annealed/cleaned cDNA was
ligated for 1 hour at room temperature into the cut/cleaned pcDNA
3.1 plasmid vector (Invitrogen) previously cut with BamHI and
HindIII. For the ligation reaction, several different ratios of
insert to vector cDNA (ranging from 25 μM :25 pM to 250 pM:25 pM
annealed cDNA) were plated. Following the ligation reaction, the
samples were heated to 65 °C for 5 min to deactivate the T4 DNA
ligase. The ligation mixture (1 μl) was electroporated into 50
 μl competent cells as described in Example 7 and the cells

immediately placed into 1 ml of SOC (Gibco). After 1 hour shaking at 37°C, 100 µl of the electroporated cells containing the minigene plasmid DNA was spread on LB/Amp plates and incubated at 37°C for 12-16 hours. To verify that insert was present, colonies were grown overnight in LB/Amp and their plasmid DNA purified (Qiagen SpinKit). The plasmid DNA was digested with Ncol (New England Biolabs, Inc.) for 1 hour at 37°C and subjected to 1.5% (3:1) agarose gel electrophoresis. Vector alone produced 3 bands. When the 56 bp annealed oligonucleotide insert is present, there is a new NcoI site resulting in a shift in the band pattern such that the digest pattern goes from three bands (3345 bp, 1352 bp, 735 bp) to four bands (3345 bp, 1011 bp, 735 bp, 380 bp). See Figure 12. DNA with the correct electrophoresis pattern was sequenced to confirm the appropriate sequence. This method may be used to insert any high affinity peptide to create a minigene constant.

Paragraph 0138, bridging pages 80 and 81:

Human embryonic kidney (HEK) 293 cells were transfected using a standard calcium phosphate procedure according to the methods of Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harpor Laboratory Press, New York, vol. 1-3 (1989), the disclosures of which are hereby incorporated by reference. To confirm the transcription of minigene constructs in transfected cells, total RNA was isolated from the cells 48 hours post transfection with pcDNA-Gαi or pcDNA-GαiR using methods known in

the art. Reverse transcriptase PCR was used to make cDNA and PCR analysis was performed using the cDNA as template with primers specific for the relevant G α carboxyl terminal peptide insert (forward: 5'-ATCCGCCGCCACCATGGGA (SEQ ID NO:[317]270); reverse: 5'-GCGAAAGGAGCGGGCGCTA (SEQ ID NO:[318]271). These primers for the G α minigenes amplify a 434 bp fragment only if the inserted peptide-encoding oligonucleotides are present; no band is observed in cells transfected with the empty pcDNA3.1 vector. The PCR products were separated on 1.5% agarose gels. The presence of a single 434 bp band indicated that G α carboxyl terminus peptide minigene RNA had been transcribed. See Figure 13. Control experiments were done using a T7 forward primer with the vector reverse primer to verify the presence of the pcDNA3.1 vector, and G3DPH primers (Clonetech) to approximate the amount of total RNA.

In the Claims:

94. (Amended) A compound identified by the method of claim 1, which comprises a peptide selected from the group consisting of SEQ ID NOS: [14, 16, 20, 22, 26, 28, 30, 32, 34, 36, 38, 40, 42, 46-105, 115-132 and 147-305] 2, 4, 6, 8, 10, 12, 13, 15, 17, 21, 23, 25-27, 30, 32, 34, 36, 38, 40, 45-85, 94-111, 125-150, 160-164, 175-178 and 183-264.

95. (Amended) A compound selected from the group consisting of SEQ ID NOS: [14, 16, 20, 22, 26, 28, 30, 32, 34, 36, 38, 40,

42, 46-105, 115-132 and 147-305] 2, 4, 6, 8, 10, 12, 13, 15, 17,
21, 23, 25-27, 30, 32, 34, 36, 38, 40, 45-85, 94-111, 125-150,
160-164, 175-178 and 183-264.

98. (Amended) A method for providing a therapeutic G protein coupled receptor signaling modifier peptide to a mammal which comprises administering to said mammal an expression construct which expresses a peptide according to SEQ ID NOS: [14, 16, 20, 22, 26, 28, 30, 32, 34, 36, 38, 40, 42, 46-105, 115-132 and 147-305] 2, 4, 6, 8, 10, 12, 13, 15, 17, 21, 23, 25-27, 30, 32, 34,
36, 38, 40, 45-85, 94-111, 125-150, 160-164, 175-178 and 183-264.